

SEQUENCE LISTING

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<120> MOLECULES INHIBITING HEPATITIS C VIRUS PROTEIN SYNTHESIS AND  
METHOD FOR SCREENING SAME

<130> 1759.200

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<151> 2003-12-11

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<151> 2002-12-12

<160> 16

<170> PatentIn version 3.1

<210> 1

<211> 326

<212> DNA

<213> Artificial Sequence

<220><221> HCV

<222> 40..372

<223> corresponds to IRES sequence of HCV

<400> 1

ctcccctgtg aagaactact gtcttcacgc agaaagcgtc tagccatggc gttagtatga	60
gtgtcgtgca gcctccagga cccccctcc cgggagagcc atagtgggtct gcggaaccgg	120
tgagtacacc ggaattgcc a ggatgaccgg gtccttttctt ggatcaaccc gctcaatgcc	180
tggagatttg ggcgtgcccc cgcgagactg ctagccgagt agtggttgggt cgcgaaaggc	240
cttgtggtac tgcctgatag ggtgcttgcg agtgccccgg gaggtctcgt agaccgtgca	300
tcatgagcac aaatcctaaa gaaaaa	326

<210> 2

<211> 80

<212> DNA

<213> Artificial Sequence

<220><221> HCV

<222> 40..119

<223> corresponds to a portion (region II) of HCV IRES sequence

<400> 2

ctccctgtg aggaactact gtcttcacgc agaaagcgtc tagccatggc gttagtatga 60

gtgttggtgca gcctccagga 80

<210> 3

<211> 37

<212> DNA

<213> Artificial Sequence

<220><221> HCV

<222> 56..92

<223> corresponds to a portion (consensus sequence) of HCV IRES sequence

<400> 3

tactgtcttc acgcagaaag cgtctagcca tggcggt 37

<210> 4

<211> 814

<212> PRT

<213> Artificial Sequence

<220><221> p116

<222> 1..814

<223> corresponds to p116 subunit of eIF3

<400> 4

Met Gln Asp Ala Glu Asn Val Ala Val Pro Glu Ala Ala Glu Glu Arg  
1 5 10 15

Ala Glu Pro Gly Gln Gln Gln Pro Ala Ala Glu Pro Pro Pro Ala Glu  
20 25 30

Gly Leu Leu Arg Pro Ala Gly Pro Gly Ala Pro Glu Ala Ala Gly Thr  
35 40 45

Glu Ala Ser Ser Glu Glu Val Gly Ile Ala Glu Ala Gly Pro Glu Pro  
50 55 60

Glu Val Arg Thr Glu Pro Ala Ala Glu Ala Glu Ala Ala Ser Gly Pro  
65 70 75 80

Ser Glu Ser Pro Ser Pro Pro Ala Ala Glu Glu Leu Pro Gly Ser His  
85 90 95

Ala Glu Pro Pro Val Pro Ala Gln Gly Glu Ala Pro Gly Glu Gln Ala  
100 105 110

Arg Asp Glu Arg Ser Asp Ser Arg Ala Gln Ala Val Ser Glu Asp Ala  
115 120 125

Gly Gly Asn Glu Gly Arg Ala Ala Glu Ala Glu Pro Arg Ala Leu Glu  
130 135 140

Asn Gly Asp Ala Asp Glu Pro Ser Phe Ser Asp Pro Glu Asp Phe Val  
145 150 155 160

Asp Asp Val Ser Glu Glu Glu Leu Leu Gly Asp Val Leu Lys Asp Arg  
165 170 175

Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val Asp Asn Val  
180 185 190

Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn Val Ile His  
195 200 205

Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe Tyr Pro Glu  
210 215 220

Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr Ala Ser Pro  
225 230 235 240

Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr Lys Leu Asp  
245 250 255

Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe Asp Lys Tyr  
260 265 270

Met Thr Ile Ser Asp Glu Trp Asp Ile Pro Glu Lys Gln Pro Phe Lys  
275 280 285

Asp Leu Gly Asn Leu Arg Tyr Trp Leu Glu Glu Ala Glu Cys Arg Asp  
 290 295 300

Gln Tyr Ser Val Ile Phe Glu Ser Gly Asp Arg Thr Ser Ile Phe Trp  
 305 310 315 320

Asn Asp Val Lys Asp Pro Val Ser Ile Glu Glu Arg Ala Arg Trp Thr  
 325 330 335

Glu Thr Tyr Val Arg Trp Ser Pro Lys Gly Thr Tyr Leu Ala Thr Phe  
 340 345 350

His Gln Arg Gly Ile Ala Leu Trp Gly Gly Glu Lys Phe Lys Gln Ile  
 355 360 365

Gln Arg Phe Ser His Gln Gly Val Gln Leu Ile Asp Phe Ser Pro Cys  
 370 375 380

Glu Arg Tyr Leu Val Thr Phe Ser Pro Leu Met Asp Thr Gln Asp Asp  
 385 390 395 400

Pro Gln Ala Ile Ile Ile Trp Asp Ile Leu Thr Gly His Lys Lys Arg  
 405 410 415

Gly Phe His Cys Glu Ser Ser Ala His Trp Pro Ile Phe Lys Trp Ser  
 420 425 430

His Asp Gly Lys Phe Phe Ala Arg Met Thr Leu Asp Thr Leu Ser Ile  
 435 440 445

Tyr Glu Thr Pro Ser Met Gly Leu Leu Asp Lys Lys Ser Leu Lys Ile  
 450 455 460

Ser Gly Ile Lys Asp Phe Ser Trp Ser Pro Gly Gly Asn Ile Ile Ala  
 465 470 475 480

Phe Trp Val Pro Glu Asp Lys Asp Ile Pro Ala Arg Val Thr Leu Met  
 485 490 495

Gln Leu Pro Thr Arg Gln Glu Ile Arg Val Arg Asn Leu Phe Asn Val  
500 505 510

Val Asp Cys Lys Leu His Trp Gln Lys Asn Gly Asp Tyr Leu Cys Val  
515 520 525

Lys Val Asp Arg Thr Pro Lys Gly Thr Gln Gly Val Val Thr Asn Phe  
530 535 540

Glu Ile Phe Arg Met Arg Glu Lys Gln Val Pro Val Asp Val Val Glu  
545 550 555 560

Met Lys Glu Thr Ile Ile Ala Phe Ala Trp Glu Pro Asn Gly Ser Lys  
565 570 575

Phe Ala Val Leu His Gly Glu Ala Pro Arg Ile Ser Val Ser Phe Tyr  
580 585 590

His Val Lys Asn Asn Gly Lys Ile Glu Leu Ile Lys Met Phe Asp Lys  
595 600 605

Gln Gln Ala Asn Thr Ile Phe Trp Ser Pro Gln Gly Gln Phe Val Val  
610 615 620

Leu Ala Gly Leu Arg Ser Met Asn Gly Ala Leu Ala Phe Val Asp Thr  
625 630 635 640

Ser Asp Cys Thr Val Met Asn Ile Ala Glu His Tyr Met Ala Ser Asp  
645 650 655

Val Glu Trp Asp Pro Thr Gly Arg Tyr Val Val Thr Ser Val Ser Trp  
660 665 670

Trp Ser His Lys Val Asp Asn Ala Tyr Trp Leu Trp Thr Phe Gln Gly  
675 680 685

Arg Leu Leu Gln Lys Asn Asn Lys Asp Arg Phe Cys Gln Leu Leu Trp  
690 695 700

Arg Pro Arg Pro Pro Thr Leu Leu Ser Gln Glu Gln Ile Lys Gln Ile  
705 710 715 720

Lys Lys Asp Leu Lys Lys Tyr Ser Lys Ile Phe Glu Gln Lys Asp Arg  
725 730 735

Leu Ser Gln Ser Lys Ala Ser Lys Glu Leu Val Glu Arg Arg Arg Thr  
740 745 750

Met Met Glu Asp Phe Arg Lys Tyr Arg Lys Met Ala Gln Glu Leu Tyr  
755 760 765

Met Glu Gln Lys Asn Glu Arg Leu Glu Leu Arg Gly Gly Val Asp Thr  
770 775 780

Asp Glu Leu Asp Ser Asn Val Asp Asp Trp Glu Glu Glu Thr Ile Glu  
785 790 795 800

Phe Phe Val Thr Glu Glu Ile Ile Pro Leu Gly Asn Gln Glu  
805 810

<210> 5

<211> 106

<212> PRT

<213> Artificial Sequence

<220><221> p116

<222> 175..279

<223> corresponds to a portion (RRM) of eIF3 p116 subunit

<400> 5

Met Asp Arg Pro Gln Glu Ala Asp Gly Ile Asp Ser Val Ile Val Val  
1 5 10 15

Asp Asn Val Pro Gln Val Gly Pro Asp Arg Leu Glu Lys Leu Lys Asn  
20 25 30

Val Ile His Lys Ile Phe Ser Lys Phe Gly Lys Ile Thr Asn Asp Phe  
35 40 45

Tyr Pro Glu Glu Asp Gly Lys Thr Lys Gly Tyr Ile Phe Leu Glu Tyr  
50 55 60

Ala Ser Pro Ala His Ala Val Asp Ala Val Lys Asn Ala Asp Gly Tyr  
65 70 75 80

Lys Leu Asp Lys Gln His Thr Phe Arg Val Asn Leu Phe Thr Asp Phe  
85 90 95

Asp Lys Tyr Met Thr Ile Ser Asp Glu Trp  
100 105

<210> 6  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..33  
<223> HCV RRM 5' primer (RRMfwd)

<400> 6

catatggatc ggccccagga agcagatgga atc

33

<210> 7  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..33  
<223> HCV RRM 3' primer (RRMrev)

<400> 7

gtgctcgagc cactcgtcac tgatcgtcac ata

33

<210> 8  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..29

<223> HCV IRES 5' primer (IRESfwd)

<400> 8

accgctagcc tcccctgtga ggaactact

29

<210> 9

<211> 46

<212> DNA

<213> Artificial Sequence

<220><221> primer\_bind

<222> 1..46

<223> HCV IRES 3' primer (IRESrev)

<400> 9

gaaagctttt ttctttgagg tttaggattt gtgctcatga tgcacg

46

<210> 10

<211> 95

<212> DNA

<213> Artificial Sequence

<220><221> primer\_bind

<222> 1..95

<223> primer IIIabcfwd which corresponds to T7 polymerase promoter +  
139-215 of HCV (regions IIIa-IIIb)

<400> 10

taatacgact cactataggg tagtgggtctg cggaaccggt gagtacaccg gaattgccag

60

gacgaccggg tcctttcttg gataaaccg ctcaa

95

<210> 11

<211> 60

<212> DNA

<213> Artificial Sequence

<220><221> primer\_bind

<222> 1..60

<223> primer IIIabcrev which corresponds to 193-252 of HCV (regions  
IIIb-IIIc)

<400> 11



tagcagtctc gcgggggcac gcccaaattct ccaggcattg agcgggttga tccaagaaag 60

<210> 12  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..20  
<223> primer T7 which corresponds to a portion of primer IIIabcfwd

<400> 12

taatacgact cactataggg 20

<210> 13  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..21  
<223> primer which corresponds to a portion of primer IIIabcrev

<400> 13

tagcagtctc gcgggggcac g 21

<210> 14  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..22  
<223> primer SP6

<400> 14

tatttaggtg acactataga at 22

<210> 15  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..27  
<223> primer Linkerrev

<400> 15

gtcctggtgg ctgcaggaca ctcatac

27

<210> 16  
<211> 48  
<212> DNA  
<213> Artificial Sequence

<220><221> primer\_bind  
<222> 1..48  
<223> primer LinkerSP6

<400> 16

tatttaggtg acactataga atactcaagc tatgcatcca acgcgttg

48